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1600

RAW SEQUENCE LISTING

DATE: 09/22/2003

PATENT APPLICATION: US/09/721,212

TIME: 10:43:44

Input Set : A:\A-451K REV 091003-54.txt

Output Set: N:\CRF4\09222003\I721212.raw

3 <110> APPLICANT: BOYLE, WILLIAM
 5 <120> TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
 7 <130> FILE REFERENCE: A-451K REV 09-10-03 54SEQ
 9 <140> CURRENT APPLICATION NUMBER: US 09/721,212
 10 <141> CURRENT FILING DATE: 2000-11-21
 12 <150> PRIOR APPLICATION NUMBER: US 09/052,521
 13 <151> PRIOR FILING DATE: 1998-03-30
 15 <150> PRIOR APPLICATION NUMBER: US 08/880,855
 16 <151> PRIOR FILING DATE: 1997-06-23
 18 <150> PRIOR APPLICATION NUMBER: US 08/842,842
 19 <151> PRIOR FILING DATE: 1997-04-16
 21 <160> NUMBER OF SEQ ID NOS: 54
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 2295
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Mus musculus
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (158)..(1105)
 33 <223> OTHER INFORMATION:

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 41 tcgcggagca gggcgcccga actccgggcg ccgcgcc atg cgc cgg gcc agc cga 175
 42 Met Arg Arg Ala Ser Arg
 43 1 5
 45 gac tac ggc aag tac ctg cgc agc tcg gag gag atg ggc agc ggc ccc 223
 46 Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro
 47 10 15 20
 49 ggc gtc cca cac gag ggt ccg ctg cac ccc gcg cct tct gca ccg gct 271
 50 Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala
 51 25 30 35
 53 ccg gcg ccg cca ccc gcc gcc tcc cgc tcc atg ttc ctg gcc ctc ctg 319
 54 Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu
 55 40 45 50
 57 ggg ctg gga ctg ggc cag gtg gtc tgc agc atc gct ctg ttc ctg tac 367
 58 Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr
 59 55 60 65 70
 61 ttt cga gcg cag atg gat cct aac aga ata tca gaa gac agc act cac 415
 62 Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His
 63 75 80 85
 65 tgc ttt tat aga atc ctg aga ctc cat gaa aac gca ggt ttg cag gac 463

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|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|------|
| 66 | Cys | Phe | Tyr | Arg | Ile | Leu | Arg | Leu | His | Glu | Asn | Ala | Gly | Leu | Gln | Asp | |
| 67 | | | | 90 | | | | | 95 | | | | | 100 | | | |
| 69 | tcg | act | ctg | gag | agt | gaa | gac | aca | cta | cct | gac | tcc | tgc | agg | agg | atg | 511 |
| 70 | Ser | Thr | Leu | Glu | Ser | Glu | Asp | Thr | Leu | Pro | Asp | Ser | Cys | Arg | Arg | Met | |
| 71 | | | 105 | | | | | 110 | | | | | 115 | | | | |
| 73 | aaa | caa | gcc | ttt | cag | ggg | gcc | gtg | cag | aag | gaa | ctg | caa | cac | att | gtg | 559 |
| 74 | Lys | Gln | Ala | Phe | Gln | Gly | Ala | Val | Gln | Lys | Glu | Leu | Gln | His | Ile | Val | |
| 75 | | 120 | | | | | 125 | | | | | 130 | | | | | |
| 77 | ggg | cca | cag | cgc | ttc | tca | gga | gct | cca | gct | atg | atg | gaa | ggc | tca | tgg | 607 |
| 78 | Gly | Pro | Gln | Arg | Phe | Ser | Gly | Ala | Pro | Ala | Met | Met | Glu | Gly | Ser | Trp | |
| 79 | 135 | | | | | 140 | | | | | 145 | | | | 150 | | |
| 81 | ttg | gat | gtg | gcc | cag | cga | ggc | aag | cct | gag | gcc | cag | cca | ttt | gca | cac | 655 |
| 82 | Leu | Asp | Val | Ala | Gln | Arg | Gly | Lys | Pro | Glu | Ala | Gln | Pro | Phe | Ala | His | |
| 83 | | | | 155 | | | | | 160 | | | | | 165 | | | |
| 85 | ctc | acc | atc | aat | gct | gcc | agc | atc | cca | tcg | ggt | tcc | cat | aaa | gtc | act | 703 |
| 86 | Leu | Thr | Ile | Asn | Ala | Ala | Ser | Ile | Pro | Ser | Gly | Ser | His | Lys | Val | Thr | |
| 87 | | | 170 | | | | | 175 | | | | | 180 | | | | |
| 89 | ctg | tcc | tct | tgg | tac | cac | gat | cga | ggc | tgg | gcc | aag | atc | tct | aac | atg | 751 |
| 90 | Leu | Ser | Ser | Trp | Tyr | His | Asp | Arg | Gly | Trp | Ala | Lys | Ile | Ser | Asn | Met | |
| 91 | | 185 | | | | | 190 | | | | | 195 | | | | | |
| 93 | acg | tta | agc | aac | gga | aaa | cta | agg | gtt | aac | caa | gat | ggc | ttc | tat | tac | 799 |
| 94 | Thr | Leu | Ser | Asn | Gly | Lys | Leu | Arg | Val | Asn | Gln | Asp | Gly | Phe | Tyr | Tyr | |
| 95 | | 200 | | | | 205 | | | | | 210 | | | | | | |
| 97 | ctg | tac | gcc | aac | att | tgc | ttt | cgg | cat | cat | gaa | aca | tcg | gga | agc | gta | 847 |
| 98 | Leu | Tyr | Ala | Asn | Ile | Cys | Phe | Arg | His | His | Glu | Thr | Ser | Gly | Ser | Val | |
| 99 | 215 | | | 220 | | | | | 225 | | | | 230 | | | | |
| 101 | cct | aca | gac | tat | ctt | cag | ctg | atg | gtg | tat | gtc | gtt | aaa | acc | agc | atc | 895 |
| 102 | Pro | Thr | Asp | Tyr | Leu | Gln | Leu | Met | Val | Tyr | Val | Val | Lys | Thr | Ser | Ile | |
| 103 | | | | 235 | | | | | 240 | | | | 245 | | | | |
| 105 | aaa | atc | cca | agt | tct | cat | aac | ctg | atg | aaa | gga | ggg | agc | acg | aaa | aac | 943 |
| 106 | Lys | Ile | Pro | Ser | Ser | His | Asn | Leu | Met | Lys | Gly | Gly | Ser | Thr | Lys | Asn | |
| 107 | | | 250 | | | | 255 | | | | | 260 | | | | | |
| 109 | tgg | tcg | ggc | aat | tct | gaa | ttc | cac | ttt | tat | tcc | ata | aat | gtt | ggg | gga | 991 |
| 110 | Trp | Ser | Gly | Asn | Ser | Glu | Phe | His | Phe | Tyr | Ser | Ile | Asn | Val | Gly | Gly | |
| 111 | | 265 | | | | 270 | | | | | 275 | | | | | | |
| 113 | ttt | ttc | aag | ctc | cga | gct | ggt | gaa | gaa | att | agc | att | cag | gtg | tcc | aac | 1039 |
| 114 | Phe | Phe | Lys | Leu | Arg | Ala | Gly | Glu | Glu | Ile | Ser | Ile | Gln | Val | Ser | Asn | |
| 115 | | 280 | | | | 285 | | | | | 290 | | | | | | |
| 117 | cct | tcc | ctg | ctg | gat | ccg | gat | caa | gat | gcg | acg | tac | ttt | ggg | gct | ttc | 1087 |
| 118 | Pro | Ser | Leu | Leu | Asp | Pro | Asp | Gln | Asp | Ala | Thr | Tyr | Phe | Gly | Ala | Phe | |
| 119 | 295 | | | 300 | | | | 305 | | | | 310 | | | | | |
| 121 | aaa | gtt | cag | gac | ata | gac | tgagactcat | ttcgtggaac | attagcatgg | | | | | | | | 1135 |
| 122 | Lys | Val | Gln | Asp | Ile | Asp | | | | | | | | | | | |
| 123 | | | | 315 | | | | | | | | | | | | | |
| 125 | atgtcctaga | tgtttgga | aaa | cttcttaaaa | aatggatgat | gtctatacat | gtgtaagact | | | | | | | | | | 1195 |
| 127 | actaagagac | atggccacg | gtgtatgaaa | ctcacagccc | tctctcttga | gcctgtacag | | | | | | | | | | | 1255 |
| 129 | gttgtgtata | tgtaaagtcc | ataggtgatg | ttagattcat | ggtgattaca | caacggtttt | | | | | | | | | | | 1315 |
| 131 | acaattttgt | aatgatttcc | tagaattgaa | ccagattggg | agaggtattc | cgatgcttat | | | | | | | | | | | 1375 |
| 133 | gaaaaactta | cacgtgagct | atggaagggg | gtcacagtct | ctgggtctaa | cccctggaca | | | | | | | | | | | 1435 |

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135 tgtgccactg agaaccttga aattaagagg atgccatgtc attgcaaaga aatgatagtg 1495
137 tgaagggtta agttcttttg aattgtttaca ttgcgctggg acctgcaaat aagttctttt 1555
139 tttctaataa ggagagaaaa atatatgtat ttttatataa tgtctaaagt tatatttcag 1615
141 gtgtaatggt ttctgtgcaa agttttgtaa attatatattg tgctatagta tttgattcaa 1675
143 aatattttaa aatgtctcac tgttgacata tttaatgttt taaatgtaca gatgtattta 1735
145 actggtgcac ttgttaattc cctgaaggt actcgtagct aagggggcag aatactgttt 1795
147 ctggtgacca catgtagttt atttctttat tctttttaac ttaatagagt cttcagactt 1855
149 gtcaaaacta tgcaagcaaa ataaataaat aaaaataaaa tgaatacctt gaataataag 1915
151 taggatgttg gtcaccaggt gcctttcaaa tttagaagct aattgacttt aggagctgac 1975
153 atagccaaaa aggatacata ataggctact gaaatctgtc aggagtattt atgcaattat 2035
155 tgaacagggtg tcttttttta caagagctac aaattgtaaa ttttgtttct tttttttccc 2095
157 atagaaaatg tactatagtt tatcagccaa aaaacaatcc actttttaat ttagtgaaag 2155
159 ttattttatt atactgtaca ataaaagcat tgtctctgaa tgtaattttt ttggtacaaa 2215
161 aaataaattt gtacgaaaac ctgaaaaaaa aaaaaaaaaa aaaaaaaagg gcggccgctc 2275
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167 <211> LENGTH: 316
168 <212> TYPE: PRT
169 <213> ORGANISM: Mus musculus
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177 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
178 20 25 30
181 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
182 35 40 45
185 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
186 50 55 60
189 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
190 65 70 75 80
193 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
194 85 90 95
197 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
198 100 105 110
201 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
202 115 120 125
205 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
206 130 135 140
209 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
210 145 150 155 160
213 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
214 165 170 175
217 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
218 180 185 190
221 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
222 195 200 205
225 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
226 210 215 220
229 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr

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230 225          230          235          240
233 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
234          245          250          255
237 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
238          260          265          270
241 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
242          275          280          285
245 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
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249 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
250 305          310          315

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256 <213> ORGANISM: Homo sapiens

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259 <221> NAME/KEY: CDS

260 <222> LOCATION: (185)..(1135)

261 <223> OTHER INFORMATION:

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269 cgcagacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gagggccgag      180
271 cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg      229
272 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser
273 1          5          10          15
275 gag gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac      277
276 Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His
277          20          25          30
279 gcc ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc      325
280 Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser
281          35          40          45
283 atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc      373
284 Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
285          50          55          60
287 gtc gcc ctg ttc ttc tat ttc aga gcg cag atg gat cct aat aga ata      421
288 Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
289          65          70          75
291 tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa      469
292 Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu
293 80          85          90          95
295 aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta      517
296 Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu
297          100          105          110
299 ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg      565
300 Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val
301          115          120          125
303 caa aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag      613
304 Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu

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| 307 | aaa gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag | 661 | | |
| 308 | Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys | | | |
| 309 | 145 150 155 | | | |
| 311 | ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc | 709 | | |
| 312 | Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile | | | |
| 313 | 160 165 170 175 | | | |
| 315 | cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg | 757 | | |
| 316 | Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg | | | |
| 317 | 180 185 190 | | | |
| 319 | ggt tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata | 805 | | |
| 320 | Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile | | | |
| 321 | 195 200 205 | | | |
| 323 | gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga | 853 | | |
| 324 | Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg | | | |
| 325 | 210 215 220 | | | |
| 327 | cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg | 901 | | |
| 328 | His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met | | | |
| 329 | 225 230 235 | | | |
| 331 | gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg | 949 | | |
| 332 | Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu | | | |
| 333 | 240 245 250 255 | | | |
| 335 | atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat | 997 | | |
| 336 | Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His | | | |
| 337 | 260 265 270 | | | |
| 339 | ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag | 1045 | | |
| 340 | Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu | | | |
| 341 | 275 280 285 | | | |
| 343 | gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag | 1093 | | |
| 344 | Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln | | | |
| 345 | 290 295 300 | | | |
| 347 | gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat | 1135 | | |
| 348 | Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp | | | |
| 349 | 305 310 315 | | | |
| 351 | tgagccccag tttttggagt gttatgtatt tcttgatgt ttggaaacat tttttaaaac | 1195 | | |
| 353 | aagccaagaa agatgtatat aggtgtgtga gactactaag aggcattggcc ccaacggtac | 1255 | | |
| 355 | acgactcagt atccatgctc ttgacctgt agagaacacg cgtattttaca gccagtggga | 1315 | | |
| 357 | gatgttagac tcatgggtgtg ttacacaatg gtttttaaat tttgtaatga attcctagaa | 1375 | | |
| 359 | ttaaaccaga ttggagcaat tacgggttga ccttatgaga aactgcatgt gggctatggg | 1435 | | |
| 361 | aggggttggg ccctggtcat gtgccccttc gcagctgaag tggagagggt gtcactagc | 1495 | | |
| 363 | gcaattgaag gatcatctga aggggcaaat tcttttgaat tgttacatca tgctggaacc | 1555 | | |
| 365 | tgcaaaaaat actttttcta atgaggagag aaaatatatg tattttttata taatatctaa | 1615 | | |
| 367 | agttatatatt cagatgtaat gttttctttg caaagtattg taaattatat ttgtgctata | 1675 | | |
| 369 | gtattttgatt caaaatattt aaaaatgtct tgctgttgac atattttaatg ttttaaatgt | 1735 | | |
| 371 | acagacatat ttaactggtg cactttgtaa attccctggg gaaaacttgc agctaaggag | 1795 | | |
| 373 | gggaaaaaaa tgttgtttcc taatatcaaa tgcagtatat ttcttcgttc tttttaagtt | 1855 | | |
| 375 | aatagatttt ttcagacttg tcaagcctgt gcaaaaaaat taaaatggat gccttgaata | 1915 | | |
| 377 | ataagcagga tgttggccac caggtgcctt tcaaatttag aaactaattg actttagaaa | 1975 | | |
| 379 | gctgacattg ccaaaaagga tacataatgg gccactgaaa tctgtcaaga gtagttatat | 2035 | | |

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L:967 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:42,Line#:964